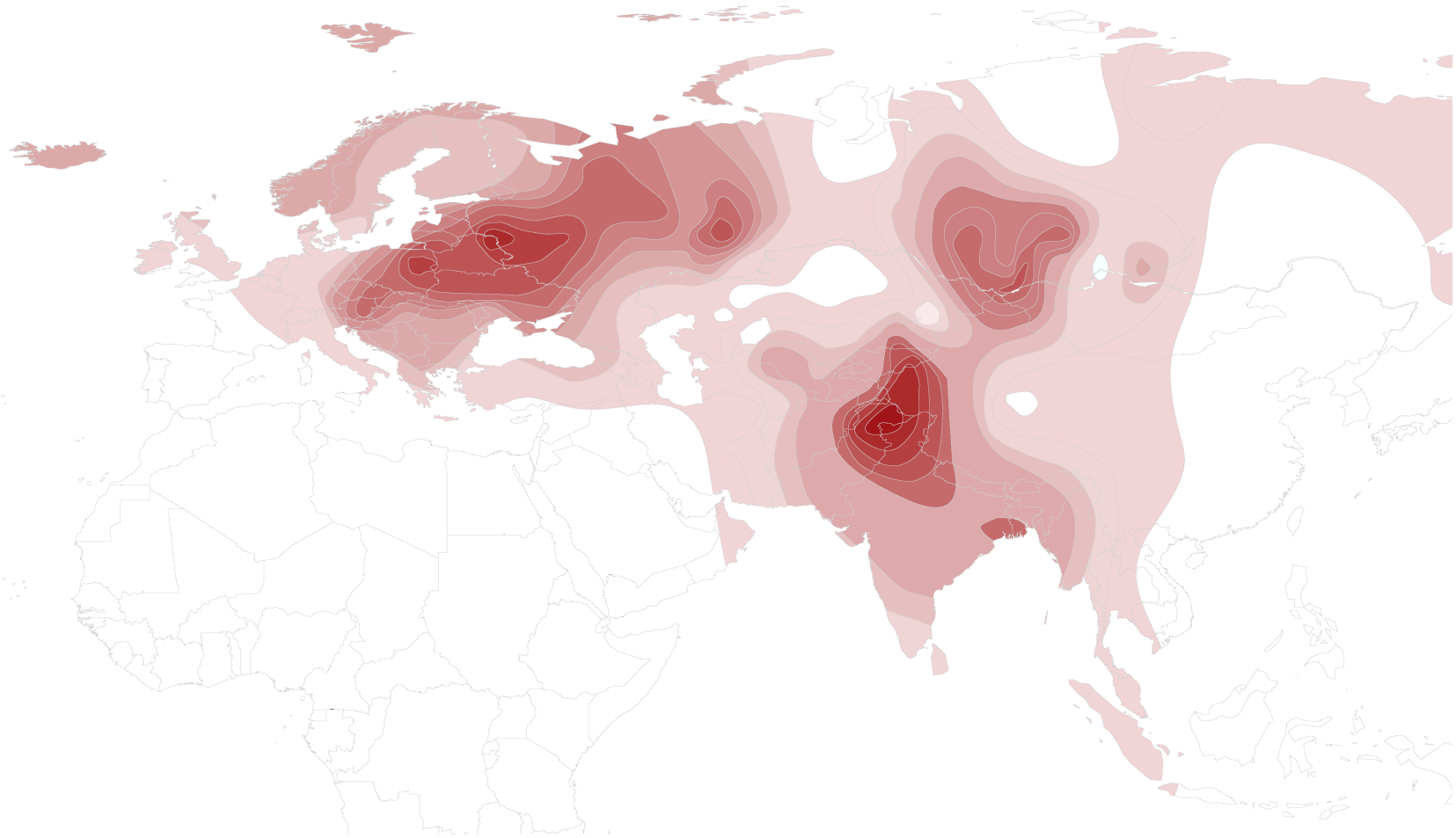


Distribution map for Y-chromosome
haplogroup R1a





:: Marker Testing ::

To determine which haplogroup you are in, your DNA was first extracted from the sample you provided. It then underwent a primary screen which looks at several SNP markers at the very top of the Y-chromosome tree. This primary panel, called Multiplex A-R, is listed below along with the secondary panels. Based upon the results of this primary screen, the secondary panel was chosen. The panels that you were tested upon are marked light blue and the markers that you were positive on shown light green.

Multiplex	A-R	AB	CD	E	FGHI	J
Region covered	All	African (for 168C samples)	Asian (for M168T/M89C/M96G samples)	African, Middle Eastern (for M96C samples)	Eurasian (for M89T/M9G/M304A samples)	Middle Eastern (for M304C samples)
Markers Tested	M9	M31	M15	DYS391	M26	M47
	M45	M32	M38	M2	M52	M67
	M89	M42	M48	M33	M170	M92
	M96	M150	M55	M35	M201	M172
	M122	M146	M125	M58	M253	M241
	M168	M182	M130	M75	P15	M267
	M175	P4	M131	M78	P16	
	M207		M145	M81	P37	
	M304		M151	M123		
	M343		M210			
	AmelXY		M217			

Multiplex	KLMN	O1	O2	PQ	R1	R2
Region covered	Eurasian (for M9C/M45G/M175+ samples)	SE-Asian (for M175-/M122T samples)	SE-Asian (for M175-/M122C samples)	Asian, Native American (for M45A/M207A samples)	Indo-European (for M207G/M343C samples)	Indo-European (for M343A samples)
Markers Tested	M5	M88	M7	M3	M17	M18
	M11	M95	M113	M19	M56	M37
	M70	M101	M117	M120	M87	M65
	M178	M103	M121	M143	M124	M126
	M214	M119	M134	M194	M157	M153
	M231	P31	M159	M199	M173	M269
	SRY9138	SRY465	M164	M242	SRY10831	P25
	Tat			M323		SRY-2627

:: Haplogroup Result ::

The testing of your sample shows that you were positive on the above highlighted markers. Additionally, you were negative on the other markers within the panels tested. Knowing this we can determine your haplogroup. An asterisk after the haplogroup would designate that branch-defining markers below the haplogroup have been tested but proved negative - e.g. I* or R1b3*

We determine you to be in Y-chromosome haplogroup **R1a1***

Haplogroup R1a is defined by marker SRY1532 plus M17 (R1a1) according to Y Chromosome Consortium (YCC) 2002 and 2003 (in earlier literature referred as haplogroup 3 by Jobling et al. 1997; Rosser et al. 2000 or Eu 19 by Semino et al. 2000) and has a vast, wide-spread distribution area on Eurasian continent. It is spread among Western Eurasian (mostly Eastern- European populations), Southern-Asian (up to 30% in Indian populations, both caste and tribal populations), Central- Asian (average 25%) and Siberian populations (20% Selkups, 22% Uygurs, 47% Altaians). The age of M17 has been approximated to about 15000 years ago (Semino et al. 2000, Wells et al. 2001).

According to data of two most comprehensive parallel surveys about European Y-chromosomal landscape by Semino et al. (2000) and Rosser et al. (2000), which both revealed similar clinal patterns for major European haplogroups, about 50% of European Y chromosomes share the M173 marker that defines R1 clade (YCC 2003). This clade consists of two separate branches harboring contrasting geographic distributions in European populations. Kivisild et al. (2003) suggested that southern and western Asia might be the source of R1 and R1a differentiation. According to Semino et al. 2000, the distribution of M173 lineages (R1) suggests that M173 is an ancient Eurasiatic marker that was brought by or arose in the group of *Homo sapiens sapiens* who entered Europe and diffused from east to west about 40 000 to 35 000 years ago, spreading the Aurignacian culture. Hg R1b shows decreasing frequency from west to east, while the second - R1a - is showing opposite frequency gradient in Europe, with its maximum frequency in Eastern Europe, particularly in Slavic populations, comprising about a half of their paternal gene pool, with highest frequencies up to nearly 60 % detected in Ukrainians and Byelorussians.

Current R1a-M17/SRY1532 distribution in Europe shows an increasing west-east frequency and variance gradients (characteristic is low frequency from 3-15% to western European populations) with peaks among Slavic (40-60%), Baltic (about 30%) and Finno-Ugric speakers (20-40%).

Besides Eastern European populations R1a is quite frequent in Scandinavian populations (20-30% in Norwegians according different datasets). In the context of North-Western Europe, mainly in case of British Isles and Iceland, the incidence of R1a is considered to be an almost unmistakable indicator of the presence of the Vikings (Helgason et al. 2000, Capelli et al. 2003). R1a occurs at 16% frequency in South-East Europe and its frequency gradient decreases slowly to the south (to 10% in Albanians, 8% in Greeks and 7% in Turks) and abruptly in the west (3% in Italians). R1a frequency and STR variance decrease in the north-south direction in South-East Europe, from 34% - 25% in mainland Croatians and Bosnians to 12% - 16% in Herzegovinians, Macedonians and Serbians.

At present level of resolution of R1a haplogroup (novel informative downstream mutations are needed to get further insight into the phylogeography of R1a in Eurasia), it is still debated what temporal and effective population size differences contributed to the spread of this haplogroup in Europe, especially as several possible episodes of gene flow may be envisioned over a long time period:

1) The spread of haplogroup R1a can be connected with post-LGM (Last Glacial Maximum) re-colonization of Europe from the Periglacial refugium in the territory of the present-day Ukraine (Semino et al. 2000),

particularly, as the highest 49a,f/Taq I haplotypes diversity of haplogroup R1a has been shown in the Ukrainians (Passarino et al. 2001).

2) An alternative possibility, linking the spread of R1a to the movement of the Kurgan people (known for the domestication of the horse) from north of the Caspian Sea in a much more recent time scale between 3000 to 1000 B.C, has been suggested by Rosser et al. (2000). This suggestion is supported by data from Zerjal et al. 2002, where the influence from East European steppes to eastern Central Asia is deduced from the pattern of the distribution of hg R1a.

3) Present distribution pattern of R1a in Eastern Europe is probably influenced also by much later migratory events already from historic times, like massive Slavic migration from 5th century AD. These migrations may possibly explain high incidence (about 30%) of R1a in Volga-Uralic region, mostly among Finno-Ugric speaking populations.

An interesting finding is the high incidence of haplogroup R1a1 (more than 50%), a non-typical hg for other Jewish communities, among Ashkenazi Levites. The possible timing and founding event of this haplogroup among Ashkenazi Levites is discussed in study by Behar et al. 2003, according to whom one possible source would be the Khazars, whose ruling class is thought to have converted to Judaism in the 8th or 9th century.

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